

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 25.3953 Seconds
(without alignments)
843.812 Million cell updates/sec

Title: US-09-622-613B-2

Perfect score: 578
Sequence: 1 ODWLTFOKKHLTNRDVCN.....TFCVTCENQAPVHVGCHC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp._archaea:*
2: sp._bacteria:*
3: sp._fungi:*
4: sp._human:*
5: sp._invertebrate:*
6: sp._mammal:*
7: sp._mhc:*
8: sp._organelle:*
9: sp._phage:*
10: sp._plant:*
11: sp._rodent:*
12: sp._virus:*
13: sp._vertebrate:*
14: sp._unclassified:*
15: sp._virus:*
16: sp._bacteriophage:*
17: sp._archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	100.0	127	13	0918V8 rana pipien
2	556	96.2	127	13	08UVX5 rana pipien
3	404.5	70.0	129	13	09DXY6 rana pipien
4	386	66.8	128	13	09DXY8 rana pipien
5	311	53.8	128	13	09DXY7 rana pipien
6	309	53.5	128	13	09DXY5 rana pipien
7	298	51.6	133	13	098SM0 rana pipien
8	292	50.5	133	13	098SM7 rana pipien
9	286	49.5	133	13	098SL9 rana pipien
10	285	49.3	132	13	098SM2 rana pipien
11	282	48.8	133	13	098SL8 rana pipien
12	280	48.4	132	13	098SM1 rana pipien
13	275.5	47.7	132	13	09DXY8 rana pipien
14	157.5	27.2	169	13	09W738 xenopus lae
15	129	22.3	152	11	09UK15 mus saxicol
16	127	22.0	157	11	09UK19 meriones un

17	126.5	21.9	153	11	09UK17 mus saxicol
18	126	21.8	157	11	09UKJ3 meriones un
19	125	21.6	157	11	09UKJ4 meriones un
20	123	21.3	154	11	09UK18 meriones un
21	122	21.1	157	11	09UKJ1 meriones un
22	121	20.9	157	11	09UKJ2 meriones un
23	120.5	20.8	155	11	09UKH9 meriones un
24	119.5	20.7	155	11	09UKH3 meriones un
25	116.5	20.2	155	11	09UK16 meriones un
26	115.5	20.0	132	6	09UK25 eulemur ful
27	115.5	20.0	155	11	09UK14 meriones un
28	115.5	20.0	170	11	09UK12 meriones un
29	114.5	19.8	150	6	09BE01 treagus ja
30	113.5	19.6	119	6	09TS06 cercopithec
31	113.5	19.6	119	6	09TV32 gorilla gor
32	113.5	19.6	132	6	09UK24 galago moho
33	113.5	19.6	155	11	09UK13 ratus norv
34	113	19.6	156	11	09UKH7 mus caroll
35	113	19.6	156	11	09UKG6 mus caroll
36	112.5	19.5	119	6	09TV30 saquinus oe
37	112.5	19.5	155	11	09UK125 mus muscul
38	112.5	19.5	155	11	09UKH8 mus pahari
39	112	19.4	124	6	09TSF2 bos taurus
40	112	19.4	156	11	09UKG7 mus caroll
41	111.5	19.3	155	11	09UKG3 mus caroll
42	111	19.2	124	6	09SNE6 bubalus bub
43	111	19.2	156	6	08S004 lemur catia
44	111	19.2	156	11	09UKH5 mus caroll
45	111	19.2	156	11	09UKH4 mus caroll

ALIGNMENTS

RESULT 1

Q918V8	PRELIMINARY:	PRT:	127 AA.
AC Q918V8;			
DT 01-OCT-2000 (TREMBLrel. 15, Created)			
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE Onconase variant rapLRI precursor.			
OS Rana pipiens (Northern leopard frog).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.			
OX NCBI_TaxID=8404;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Liver.			
RX MEDLINE=20330357; PubMed=10871370;			
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V., Rybak S.M.;			
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a			
RT 3' UTR of unusual length and structure.";			
RL Nucleic Acids Res. 28:2375-2382(2000).			
DR EMBL: AF165133; AAF76935.1;			
DR HSSP: P22069; IONC.			
DR InterPro: IPR001427; RNaseA.			
DR Pfam: PF00074; RNaseA.1.			
DR ProDom: PD000535; RNaseA.1.			
DR SMART: SM00092; RNase_PC.1.			
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
KW SIGNAL.			
FT SIGNAL. 1 23 POTENTIAL.			
SQ SEQUENCE 127 AA; 14491 MW; B851IDC5407AB69B CRC64;			
QY Query Match 100.0%; Score 578; DB 13; Length 127;			
Best Local Similarity 100.0%; Pred. No. 3e-58;			
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

QY 1 ODWLTFOKKHLTNRDVCNINIMSTNFFHCKDKNTFIYSPEPYKAKCKIIISKVLT 60
Db 24 ODWLTFOKKHLTNRDVCNINIMSTNFFHCKDKNTFIYSPEPYKAKCKIIISKVLT 83

OY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
 DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 2

ID 08UVX5 PRELIMINARY: PRT: 127 AA.
 AC 08UVX5;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Onconase precursor.
 GN RPR.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liao Y.-D., Wang S.-C.;
 RT "Rana pipiens onconase genomic DNA."
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF332139; ANL54383.1;
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL. 1 23 POTENTIAL.
 SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;
 Query Match
 Best Local Similarity 96.2%; Score 556; DB 13; Length 127;
 Matches .100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAICGIIASKNVLT 60
 DB 24 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAICGIIASKNVLT 83
 OY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
 DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 3
 O9DFY6 PRELIMINARY: PRT: 129 AA.
 AC 09DFY6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNaseA ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue-Liver.
 RX MEDLINE-20512555; PubMed-11058105;
 RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog)."
 RL Nucleic Acids Res. 28:4097-4104(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Tissue-Liver.
 RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF424255; AAG31441.2;
 DR HSP: P22069; IONC.

DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL. 1 23 POTENTIAL.
 SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match
 Best Local Similarity 70.0%; Score 404.5; DB 13; Length 129;
 Matches .71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

OY 1 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAICGIIASKNVLT 60
 DB 24 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAICGIIASKNVLT 83
 OY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
 DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 4

ID 09DFY8 PRELIMINARY: PRT: 128 AA.
 AC 09DFY8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNaseA ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue-Liver.
 RX MEDLINE-20512555; PubMed-11058105;
 RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog)."
 RL Nucleic Acids Res. 28:4097-4104(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Tissue-Liver.
 RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF242553; AAG31439.1;
 DR HSP: P22069; IONC.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL. 1 23 POTENTIAL.
 SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match
 Best Local Similarity 66.8%; Score 386; DB 13; Length 128;
 Matches .70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

OY 1 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAICGIIASKNVLT 60
 DB 24 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAICGIIASKNVLT 83
 OY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
 DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

ID	Q9DFY7	PRELIMINARY:	PRT:	128 AA.
AC	Q9DFY7			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	RC-RNase3 ribonuclease precursor.			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_TaxID=8440;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER:			
RC	MEDLINE=20512555; PubMed=11058105;			
RA	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;			
RT	"Purification and cloning of cytotoxic ribonucleases from Rana			
RT	catesbeiana (bullfrog).";			
RL	Nucleic Acids Res. 28:4097-4104(2000).			
DR	EMBL; AF242554; AAC31440.2;			
DR	HSSP; P22069; IONC			
DR	InterPro; IPR001427; RNaseA.			
DR	Pfam; PF00074; RNaseA; 1.			
DR	ProDom; PD000355; RNaseA; 1.			
DR	SMART; SM00092; RNase_Pc; 1.			
DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
FW	Signal.			
FT	SIGNAL	1	23	POTENTIAL.
FT	CHAIN	24	128	RC-RNASE3 RIBONUCLEASE.
SO	SEQUENCE	128 AA;	14517 MW;	2b14986082E0587D CRC64;
QY	Query Match	53.8%;	Score 311;	DB 13; Length 128;
Db	Best Local Similarity	54.8%;	Pred. No. 8.2e-28;	
Db	Matches	57;	Conservative 12;	Mismatches 35; Indels 0; Gaps 0
QY	1	QDMLTFOKHLTNRDQDCNNIMTNLFHCKDKNTFIYSRPEVKAICGIIASNNVLT	60	
Db	24	QDMETFOKHLTDTRKVCQDVEMAKALPDKCKTNTFIYALPGRYKALCKNIFDNDVL	83	
QY	61	SEFISDCNVTSPCKYKLYKSKTNTFCYTCENQAPVHVGVGHC	104	
Db	84	DAFLPQCCKRIKLPCHRYKLSSTNTITCTCYNOLPIHFGVQSC	127	
RESULT 6				
ID	Q9DFY5	PRELIMINARY:	PRT:	128 AA.
AC	Q9DFY5			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	RC-RNase6 ribonuclease precursor.			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_TaxID=8440;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER:			
RC	MEDLINE=20512555; PubMed=11058105;			
RA	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;			
RT	"Purification and cloning of cytotoxic ribonucleases from Rana			
RT	catesbeiana (bullfrog).";			
RL	Nucleic Acids Res. 28:4097-4104(2000).			
DR	EMBL; AF242556; AAC31442.2;			
DR	HSSP; P22069; IONC			
DR	InterPro; IPR001427; RNaseA.			

[illegible]

CN	RCR.
OS	Rana catesbeiana (Bull frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Ampibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX	NCHI_taxid=8400;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LIVER:
RX	MEDLINE=98165825; PubMed=9497370;
RA	Huang H.C., Wang S.C., Liu Y.J., Lu S.C., Liao Y.D.;
RT	"The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RL	Tissue distribution, cloning, purification, cytotoxicity, and active
RD	residues for RNase activity.";
RL	J. Biol. Chem. 273:6395-6401(1998).
DR	EMBL: AF039104; AAD10702.1; --
DR	HSSP; P11916; IBC4.
DR	InterPro: IPRO01427; RNASEA.
DR	Pfam: PF00074; rnasea; 1.
DR	Prodrom: PD000535; RNaseA; 1.
DR	SMART: SM00092; RNase_Pc; 1.
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW	Signal.
FT	SIGNAL 1 22 POTENTIAL.
FT	CHAIN 23 133 RIBONUCLEASE.
SO	SEQUENCE 133 AA; 14762 MW; ATD62594FTD16FOC CRC64;

Query Match	50.5%;	Score 292;	DB 13;	Length 133;
Best local Similarity	49.5%;	Pred. No. 1.2e-25;		
Matches 55;	Conservative 16;	Mismatches 35;	Indels 8;	Gaps 3

OY 1 ODWLTFFKKHLLTNRDVDCNNINISTNLF----CHCKQFPIFYRPREDEVALKGLGIIASNN 56
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 23 QNMATFPQKHILNIPIICMTIMDMNNIYLGGCKRKNTFIISATTVAKLCTGVLI--NNN 81

OY 57 VLTISEEYLSDC---NWTSRPCKTKLKKSNITFCYCENQAPHYGVGHC 104
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 82 VLSTTRQLNTCTRTSLTPPRCPSSSTEENNYLCVKENQDYPVPHFGIGTGC 132

RESULT 9			
ID	Q98SL9	PRELIMINARY:	PRT: 133 AA.
AC	Q98SL9		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	RNase A-type ribonuclease rc212 precursor.		
OS	Rana catesbeiana (Bull frog).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.		
OX	NCBI_TaxId=8400;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21539506; PubMed=11683320;		
RT	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;		
RT	"Rapid diversification of RNase A superfamily ribonuclease from the		
RL	bullfrog, Rana catesbeiana.,"		
RL	J. Mol. Evol. 53:31-38(2001).		
DR	EMBL; AF351210; AAK30256.1; -		
DR	HSSP; P11916; 1BC4.		
DR	InterPro; IPR001427; RNaseA.		
DR	Pfam; PF00074; rnasea.1.		
DR	ProDom; PD000535; RNaseA; 1.		
DR	SMART; SM00092; RNase_Fc; 1.		
DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.		
KW	Signal.		
FT	SIGNAL	1	22
FT	SEQUENCE	133 AA;	14615 MW; C8785B236B2654E CRC64;
			POTENTIAL.
Query Match		49.5%;	Score 286; DB 13; Length 133;
Best Local Similarity		47.7%;	Pred. No. 6e-25;
Matches	53; Conservative	17; Mismatches	33; Indels
			8; Gaps
			3;

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QY      1  ODLLTPCKKHLTHRDVDCNNIMSTNLF-----HCKOKNFETSRPREPPALCKGIASN 50
QY      2  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      23  QNAAITFPCKKHTNTSSINCNSIMNNSLYIYGCGCKAVNFIFIASATTYVAGICSG-VTDK 81

QY      57  VLTTSFYLSDCN--VTSRPCKRYKLLKSTNFCVTCENADPVHFGVCHC 104
Db      82  VLSSTKQLDICTRIFLTTPRRCPSSTETNLYICVCCENADPVHFGISDC 132

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ID	Q98SM2	PRELIMINARY:	PRT:	132 AA.
AC	Q98SM2;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Rnase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).			
OS	Rana catesbeiana (Bull frog).			
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranae.			
NCBI_TaxID	8400;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21539506; PubMed=11683320;			
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;			
RT	"Rapid diversification of Rnase A superfamily ribonuclease from the			
RL	bullfrog, Rana catesbeiana.";			
RL	J. Mol. Evol. 53:31-38(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RL	Liao Y.-D., Tang P.-C., Jeng J.-T.;			
RA	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF351207; AAK30253.1; -			
DR	EMBL; AF359578; AAL87036.1; -			
DR	HSSP; P11916; lBC4.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam; PF00074; rnasea; 1.			
DR	Prodom; PD000535; RNaseA; 1.			
DR	SMART; SM00092; RNase_Pc; 1.			
DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
KT	Signal.			
RR				
FT	SIGNAL	1	22	POTENTIAL.
FT	CHAIN	23	132	RC-RNASE7.
SO	SEQUENCE	132 AA;	14412 MW;	131AV45187978687 CRC64;

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Query_Match 49.3%; Score 285; DB 13; Length 132;
Best Local Similarity 47.7%; Pred. No. 7.7e-25;
Matches 53; Conservative 14; Mismatches 36; Indels 8; Gaps 3;

OY 1 ODWLTFQKHLLTNRDVCNNIMSTNLF---HCKDKKTFIYSRPEYKAICGIIASKN 56
   | | | | | : | : | : | | : | | | | | | | | | | | | | | | | | |
Db 23 QTMAKFQGGKHLPISISSICNTIMDNNIIIVGGQCKKNTFIISATYTKALCNG-VYNSN 81
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 57 VLTTSSEYPLSDC---NWTSRPCKYKLLKSTNTECVTCENQAPVHPVGYGHC 104
   | | | | | : | : | | | | | | | | | | | | | | | | | | | | | |
Db 82 VLSEPTREFLDCTRTSITRPCCPYSSKKEKNKICVCKENQLPVHFAGIGKC 132
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
O98SL8 PRELIMINARY; PRT; 133 AA.
AC O98SL8;
DT 01-JUN-2001 (TremBLrel. 17, created)
DT 01-JUN-2001 (TremBLrel. 19, last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, last annotation update)
DE RNase A-type ribonuclease rcz18 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE-21539506; PubMed-11683320;
RA Rosenbery H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of Rnase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351211; AAK30257.1; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR Prodom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;

Query Match 48.8%; Score 282; DB 13; Length 133;
Best Local Similarity 46.8%; Pred. No. 1.7e-24;
Matches 52; Conservative 18; Mismatches 33; Indels 8; Gaps 3;

QY 1 QDWLTFQKKHLNTRDVDCNNINSTNLF---HCKDKNTFYSPREPVKATCKGIISKN 56
DB 23 QNATFPOQHITNTSSINCNSINMNSLYIGGCKKNTFTIASSATTYKIGICSG-VTDK 81
QY 57 VLTSEFYISDCN--VTSRPCKYKLRKSTNTPFCVTCENQAPVHFVGHC 104
DB 82 VLSTTRFOLDICTRIFITPRCPYSSRTENYICVCKENQCPVHFAGIGKC 132

RESULT 12
Q98SM1 ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Rnase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21539506; PubMed-11683320;
RA Rosenbery H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of Rnase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351208; AAK30254.1; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR Prodom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 48.4%; Score 280; DB 13; Length 132;
Best Local Similarity 46.8%; Pred. No. 2.9e-24;
Matches 54; Conservative 14; Mismatches 35; Indels 8; Gaps 3;

QY 1 QDWLTFQKKHLNTRDVDCNNINSTNLF---HCKDKNTFYSPREPVKATCKGIISKN 56
DB 23 QNATFPOQHITNTSSINCNSINMNSLYIGGCKKNTFTIASSATTYKATCTVLSN-N 81
QY 57 VLTSEFYISDCN--VTSRPCKYKLRKSTNTPFCVTCENQAPVHFVGHC 104
DB 82 VLSTTRFOLDXXTRFTITSRCPYSSRTENYICVCKENQCPVHFAGIGKC 132

RESULT 13

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Q9DF78 ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RC-RnaseI ribonuclease precursor.
DE Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE-20512555; PubMed-11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytototoxic ribonucleases from Rana
RT catesbeiana (bullfrog)."
Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF288642; AAG30414.2; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR Prodom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;

Query Match 47.7%; Score 275.5; DB 13; Length 132;
Best Local Similarity 44.1%; Pred. No. 9.4e-24;
Matches 49; Conservative 19; Mismatches 36; Indels 7; Gaps 2;

QY 1 QDWLTFQKKHLNTRDVDCNNINSTNLF---HCKDKNTFYSPREPVKATCKGIISKN 56
DB 22 QNMAKFEKHLTSTSSIDCNTIMDKAIYIGCKEKERTFTISSEDDWKAICSCVSPDRK 81
QY 57 VLTSEFYISDCN--NVTSPCKYKLRKSTNTPFCVTCENQAPVHFVGHC 104
DB 82 ELSTTSFKLNTCINDSTITPRCPYHPSDNNKICVCKEKQLPVHFVGIGKC 132

RESULT 14
Q9W738 ID Q9W738 PRELIMINARY; PRT; 169 AA.
AC Q9W738;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FRL2 protein.
GN FRL2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96069863; PubMed-7585965;
RA Kinoshita N., Minshull J., Kirschner M.W.;
RT "The identification of two novel ligands of the FGF receptor by a
RT yeast screening method and their activity in Xenopus development."
Cell 83:621-630(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Kinoshita N., Kirschner M.W.;

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